

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/23 06:44:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504413.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR504413 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504413_1.fastq.gz SRR504413_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Jun 23 06:44:31 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504413.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	142,220,378
Mapped reads	135,374,488 / 95.19%
Unmapped reads	6,845,890 / 4.81%
Mapped paired reads	135,374,488 / 95.19%
Mapped reads, first in pair	67,755,584 / 47.64%
Mapped reads, second in pair	67,618,904 / 47.55%
Mapped reads, both in pair	134,987,664 / 94.91%
Mapped reads, singletons	386,824 / 0.27%
Secondary alignments	0
Supplementary alignments	2,201,462 / 1.55%
Read min/max/mean length	30 / 100 / 99.63
Duplicated reads (estimated)	57,953,035 / 40.75%
Duplication rate	28.66%
Clipped reads	68,301,721 / 48.03%

2.2. ACGT Content

Number/percentage of A's	3,857,785,229 / 29.73%
Number/percentage of C's	2,621,360,406 / 20.2%
Number/percentage of T's	3,853,961,384 / 29.7%
Number/percentage of G's	2,631,299,411 / 20.28%
Number/percentage of N's	9,928,360 / 0.08%

GC Percentage	40.49%
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2.3. Coverage

Mean	4.1925
Standard Deviation	49.2288

2.4. Mapping Quality

Mean Mapping Quality	50.56
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2.5. Insert size

Mean	75,295.18
Standard Deviation	2,622,633.72
P25/Median/P75	128 / 156 / 186

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	66,090,974
Insertions	1,197,109
Mapped reads with at least one insertion	0.88%
Deletions	2,498,112
Mapped reads with at least one deletion	1.82%
Homopolymer indels	46.63%

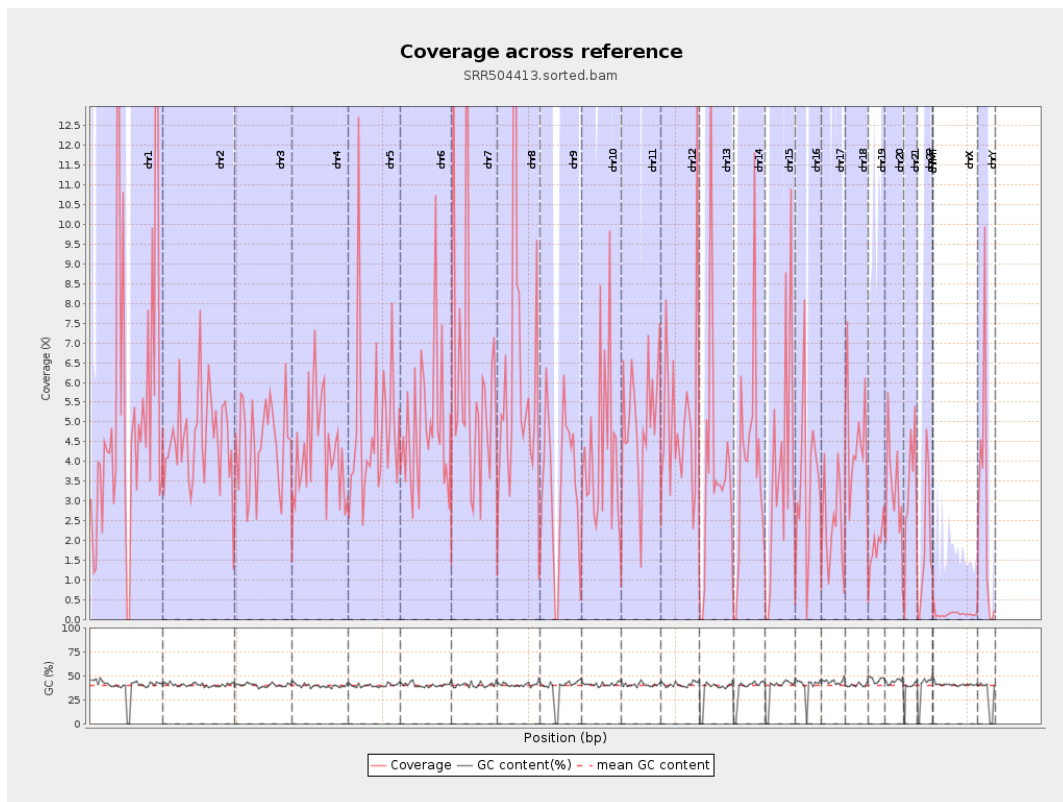
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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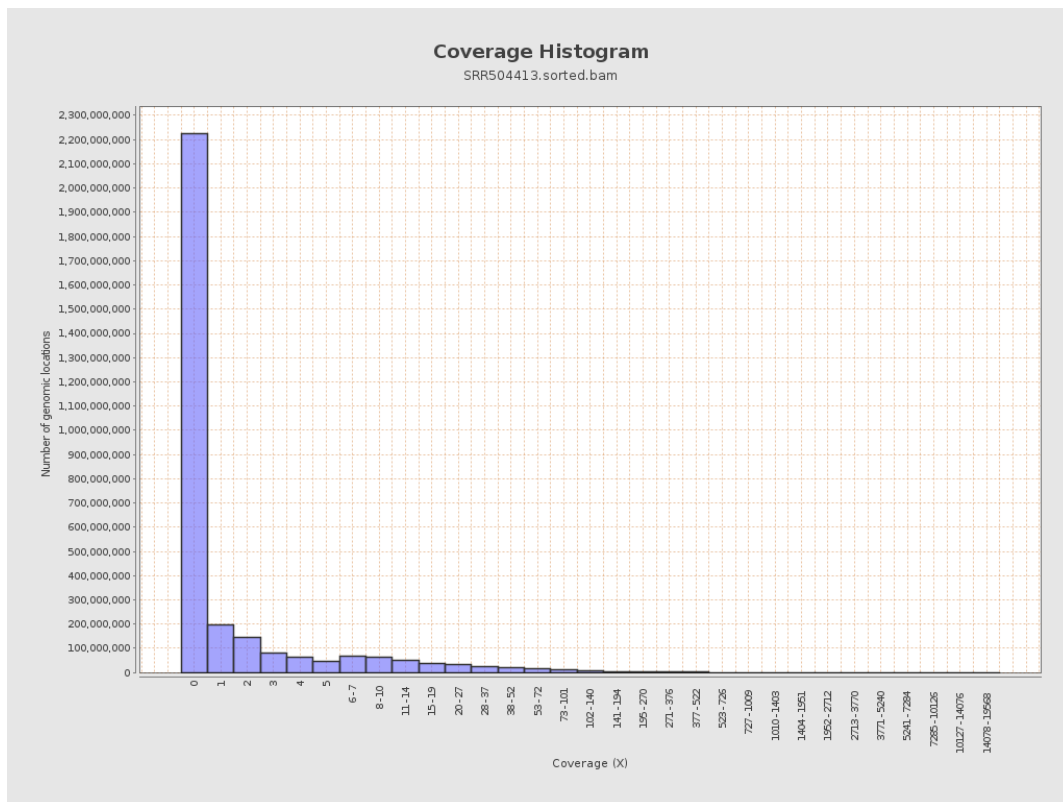
		bases	coverage	deviation
chr1	249250621	1294747104	5.1946	89.9796
chr2	243199373	1105898859	4.5473	25.9781
chr3	198022430	881619856	4.4521	23.3573
chr4	191154276	822140458	4.3009	25.2849
chr5	180915260	875413330	4.8388	39.8583
chr6	171115067	828789459	4.8435	38.6998
chr7	159138663	983251877	6.1786	88.5374
chr8	146364022	884322147	6.0419	81.9949
chr9	141213431	497309883	3.5217	22.6293
chr10	135534747	579263119	4.2739	40.3065
chr11	135006516	679665435	5.0343	37.3476
chr12	133851895	683572619	5.1069	64.0279
chr13	115169878	427314541	3.7103	46.7853
chr14	107349540	432917743	4.0328	51.566
chr15	102531392	381615346	3.7219	57.7412
chr16	90354753	307111036	3.3989	40.3418
chr17	81195210	199563395	2.4578	15.864
chr18	78077248	353402476	4.5263	36.4722
chr19	59128983	110693545	1.8721	11.2465
chr20	63025520	207896471	3.2986	23.9666
chr21	48129895	155380806	3.2284	24.5212
chr22	51304566	98772364	1.9252	16.1412
chrMT	16571	576	0.0348	0.3045
chrX	155270560	21944042	0.1413	1.9403

chrY	59373566	165945989	2.7949	26.7146
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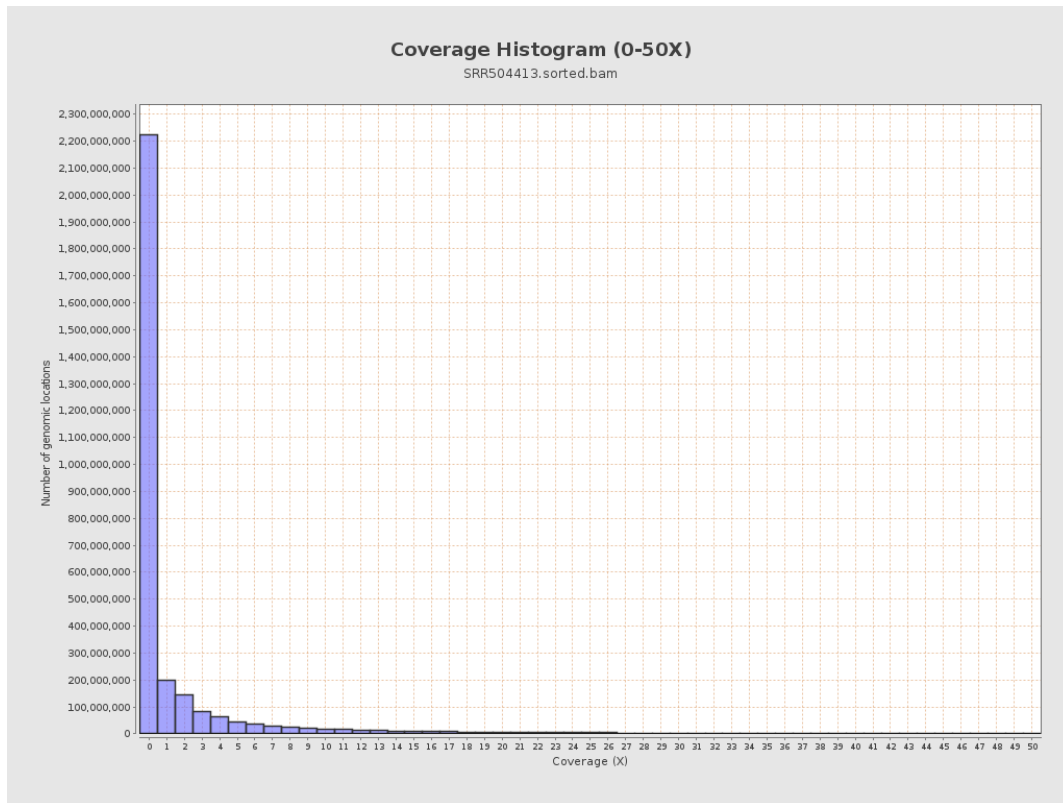
3. Results : Coverage across reference



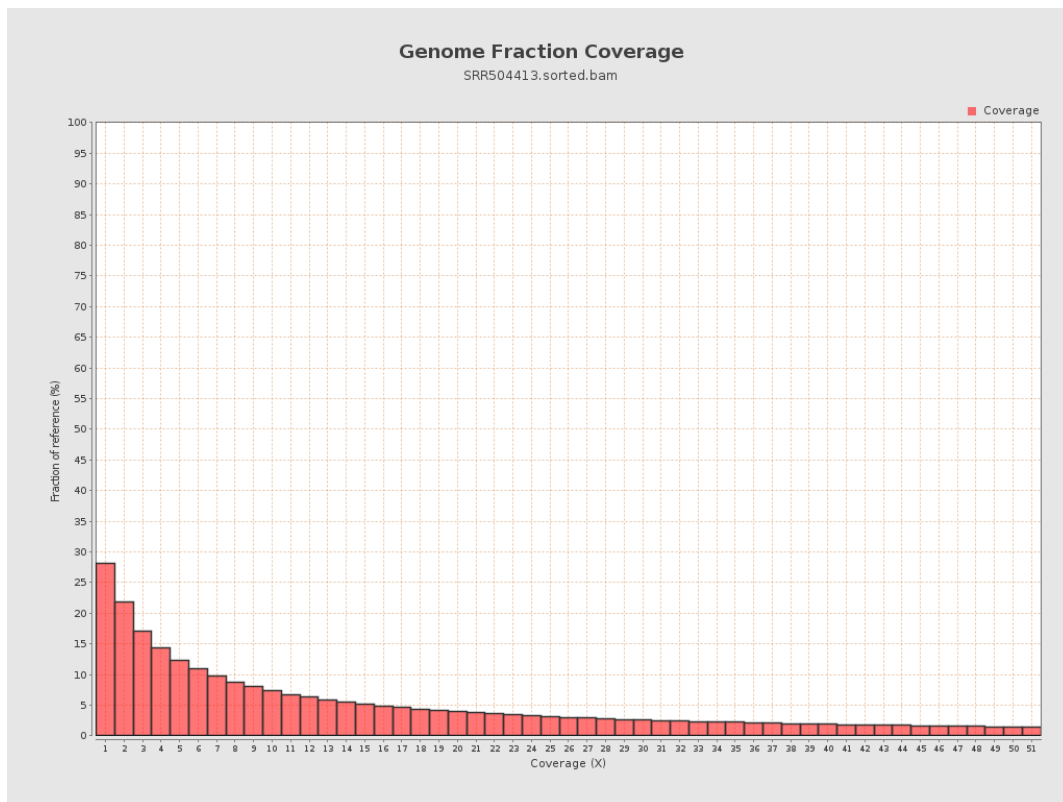
4. Results : Coverage Histogram



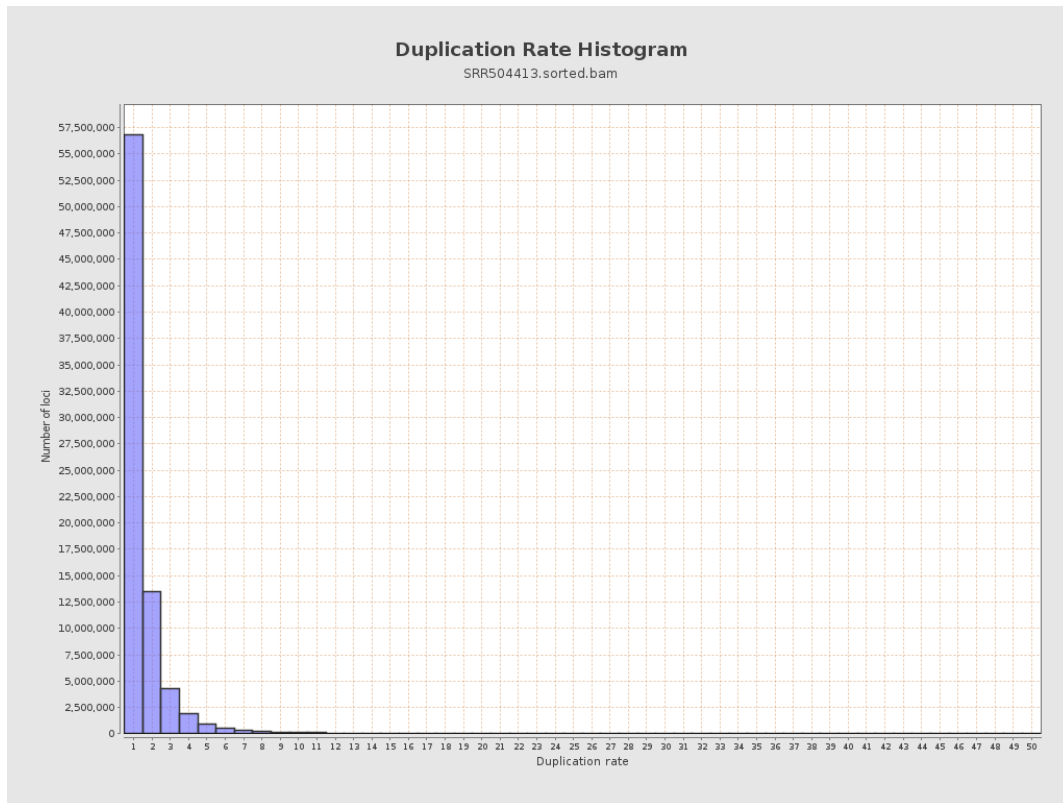
5. Results : Coverage Histogram (0-50X)



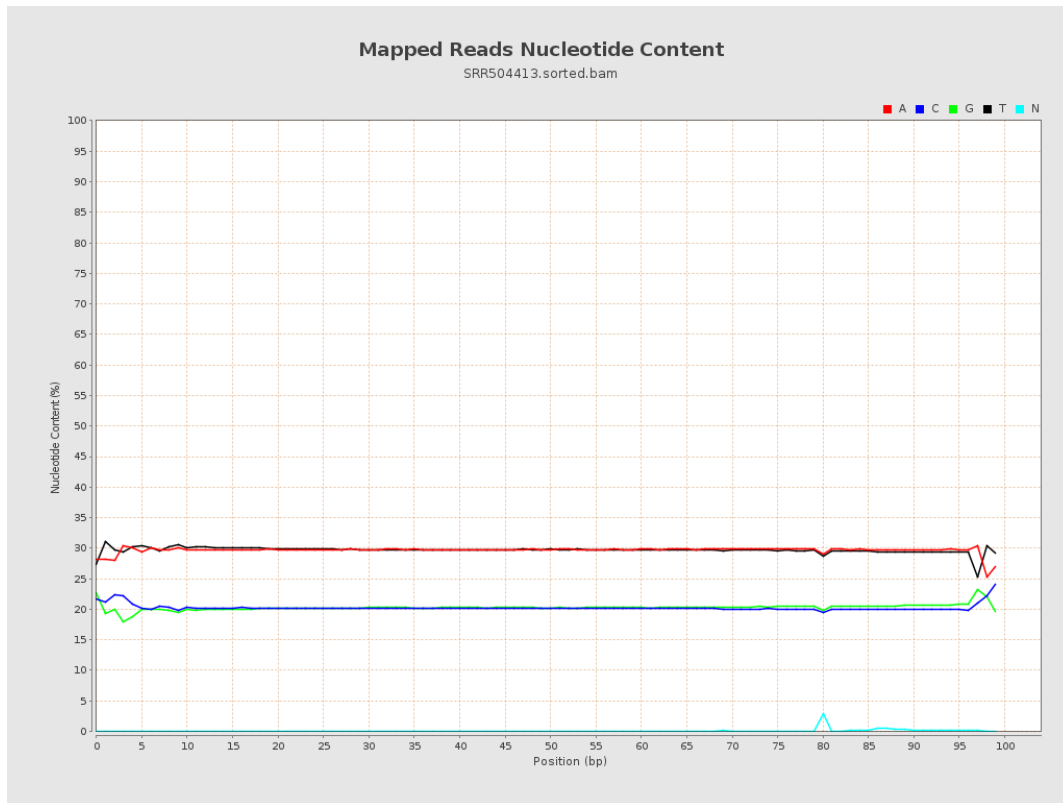
6. Results : Genome Fraction Coverage



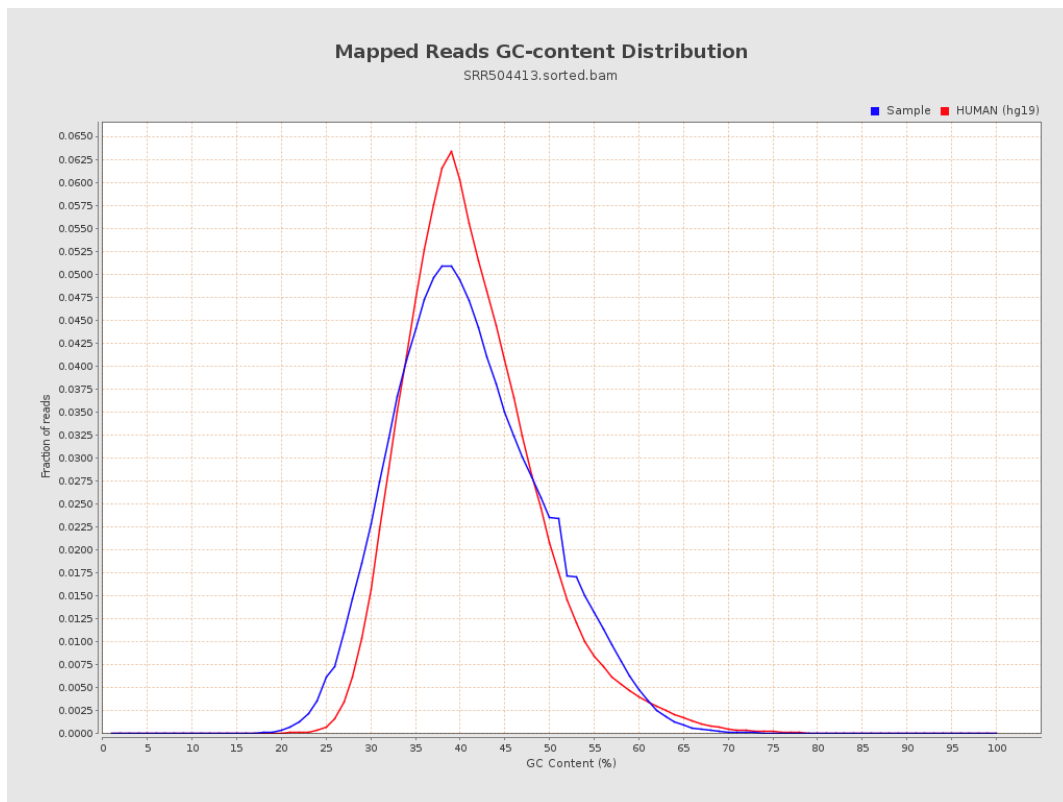
7. Results : Duplication Rate Histogram



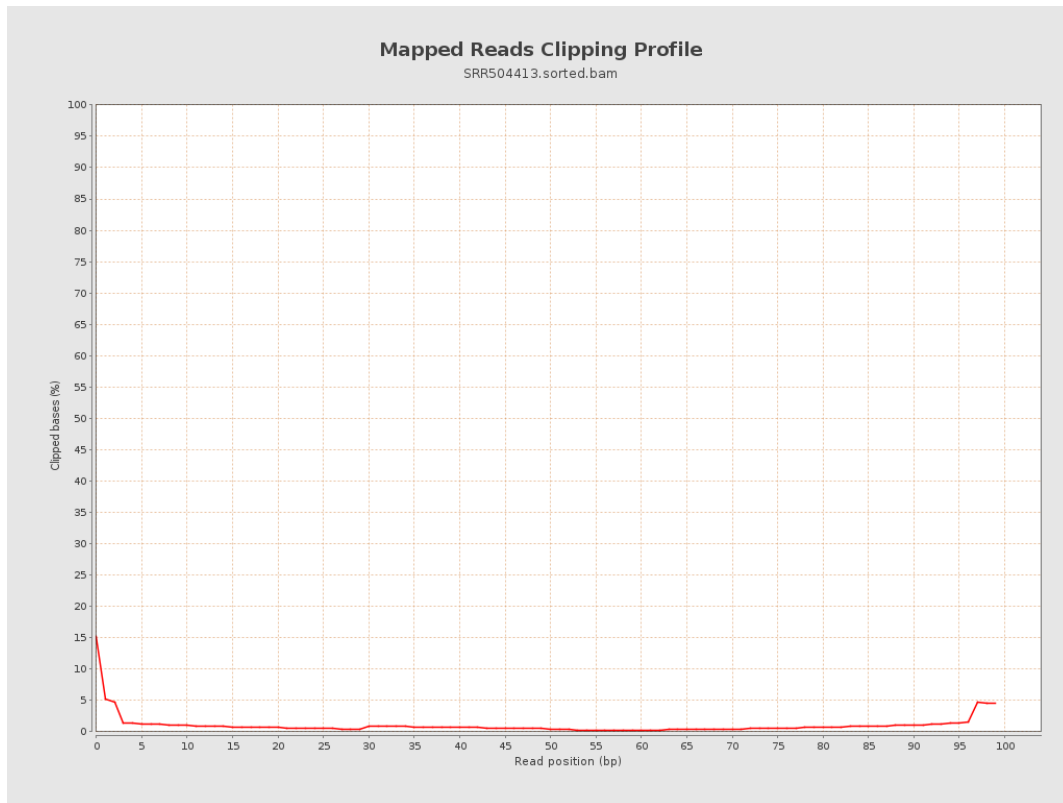
8. Results : Mapped Reads Nucleotide Content



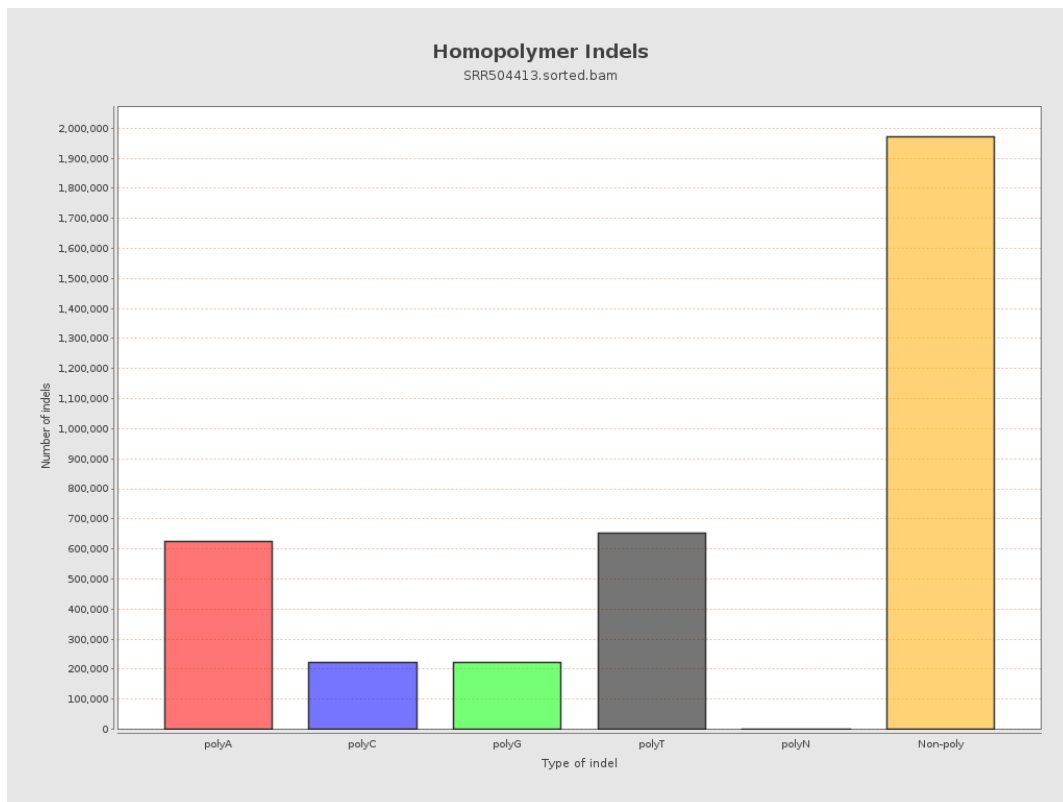
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



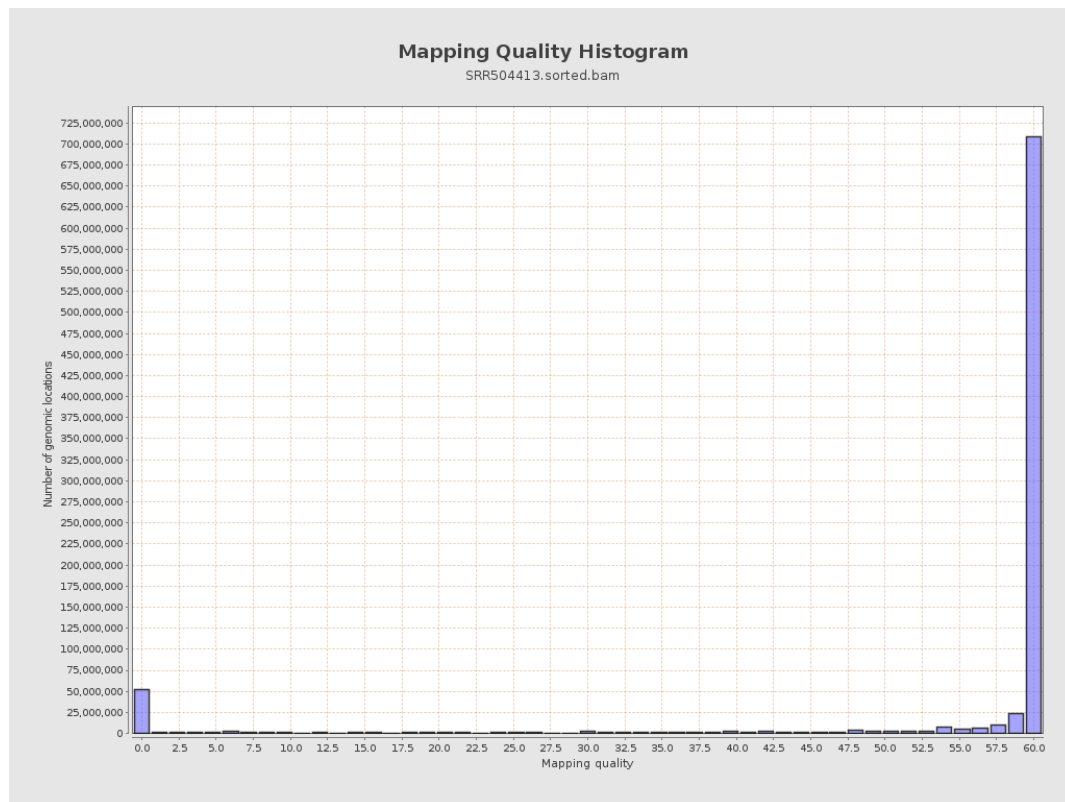
11. Results : Homopolymer Indels



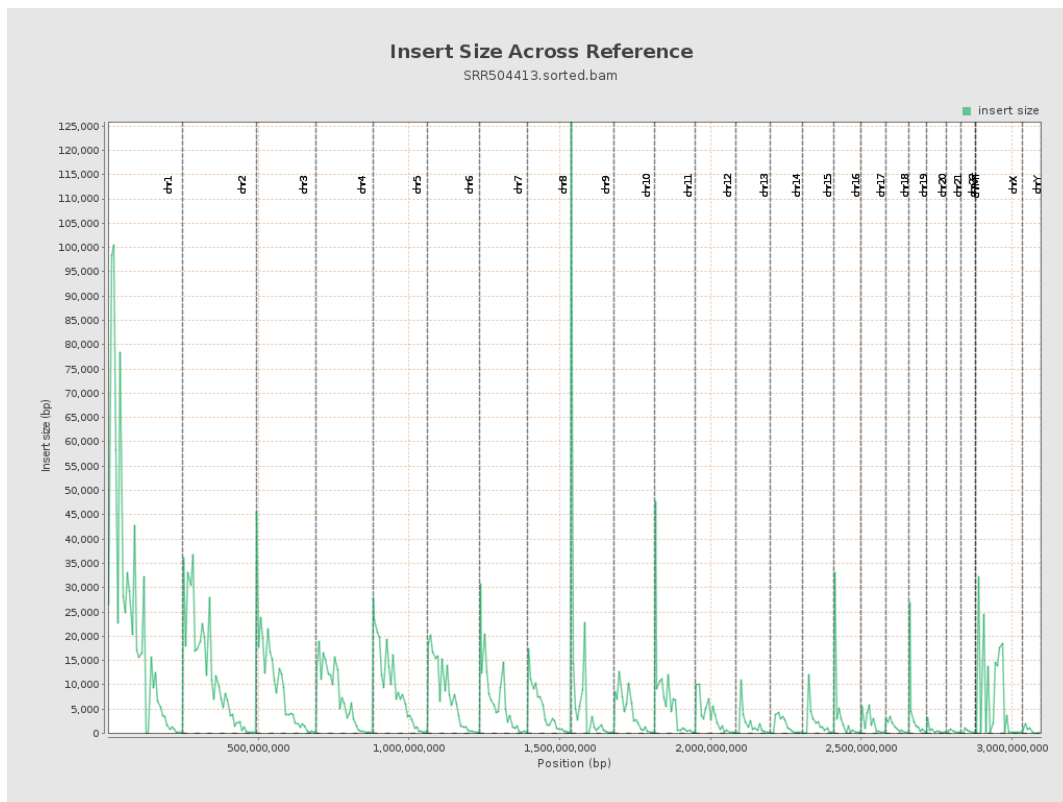
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

